

**10/574045**

## SEQUENCE LISTING

&lt;110&gt; CHUGAI SEIYAKU KABUSHIKI KAISHA

&lt;120&gt; PROTEIN EXPRESSED IN NK CELL

&lt;130&gt; C1-A0308P

&lt;150&gt; JP 2003-338331

&lt;151&gt; 2003-09-29

&lt;160&gt; 53

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 1473

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (87)..(1376)

&lt;223&gt;

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Gly Lys Thr Val Trp Leu Tyr Leu Gln Ala Trp Pro Asn Pro Val Phe

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Glu Gly Asp Ala Leu Thr Leu Arg Cys Gln Gly Trp Lys Asn Thr Pro	
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ctg tct cag gtg aag ttc tac aga gat gga aaa ttc ctt cat ttc tct	257
Leu Ser Gln Val Lys Phe Tyr Arg Asp Gly Lys Phe Leu His Phe Ser	
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aag gaa aac cag act ctg tcc atg gga gca gca aca gtg cag agc cgt	305
Lys Glu Asn Gln Thr Leu Ser Met Gly Ala Ala Thr Val Gln Ser Arg	
60 65 70	
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Gly Gln Tyr Ser Cys Ser Gly Gln Val Met Tyr Ile Pro Gln Thr Phe	
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aca caa act tca gag act gcc atg gtt caa gtc caa gag ctg ttt cca	401
Thr Gln Thr Ser Glu Thr Ala Met Val Gln Val Gln Glu Leu Phe Pro	
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cct cct gtg ctg agt gcc atc ccc tct cct gag ccc cga gag ggt agc	449
Pro Pro Val Leu Ser Ala Ile Pro Ser Pro Glu Pro Arg Glu Gly Ser	
110 115 120	
ctg gtg acc ctg aga tgt cag aca aag ctg cac ccc ctg agg tca gcc	497
Leu Val Thr Leu Arg Cys Gln Thr Lys Leu His Pro Leu Arg Ser Ala	
125 130 135	
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Leu Arg Leu Leu Phe Ser Phe His Lys Asp Gly His Thr Leu Gln Asp	
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agg ggc cct cac cca gaa ctc tgc atc ccg gga gcc aag gag gga gac	593
Arg Gly Pro His Pro Glu Leu Cys Ile Pro Gly Ala Lys Glu Gly Asp	
155 160 165	

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Lys Gln Ser Pro Gln Leu Glu Val Arg Val Gln Ala Pro Val Ser Arg  
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cct gtg ctc act ctg cac cac ggg cct gct gac cct gct gtg ggg gac 737  
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atg gtg cag ctc ctc tgt gag gca cag agg ggc tcc cct ccg atc ctg 785  
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220 225 230

tat tcc ttc tac ctt gat gag aag att gtg ggg aac cac tca gct ccc 833  
Tyr Ser Phe Tyr Leu Asp Glu Lys Ile Val Gly Asn His Ser Ala Pro  
235 240 245

tgt ggt gga acc acc tcc ctc ctc ttc cca gtg aag tca gaa cag gat 881  
Cys Gly Gly Thr Thr Ser Leu Leu Phe Pro Val Lys Ser Glu Gln Asp  
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gct ggg aac tac tcc tgc gag gct gag aac agt gtc tcc aga gag agg 929  
Ala Gly Asn Tyr Ser Cys Glu Ala Glu Asn Ser Val Ser Arg Glu Arg  
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agt gag ccc aag aag ctg tct ctg aag ggt tct caa gtc ttg ttc act 977  
 Ser Glu Pro Lys Lys Leu Ser Leu Lys Gly Ser Gln Val Leu Phe Thr  
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Lys Ala Gly Pro Leu Pro Ser Gln Ile Pro Pro Thr Ala Pro Gly Gly	
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Glu Gln Cys Pro Leu Tyr Ala Asn Val His His Gln Lys Gly Lys Asp	
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Glu Gly Val Val Tyr Ser Val Val His Arg Thr Ser Lys Arg Ser Glu	
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gcc agg tct gct gag ttc acc gtg ggg aga aag gac agt tct atc atc	1265
Ala Arg Ser Ala Glu Phe Thr Val Gly Arg Lys Asp Ser Ser Ile Ile	
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Cys Ala Glu Val Arg Cys Leu Gln Pro Ser Glu Val Ser Ser Thr Glu	
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Val Asn Met Arg Ser Arg Thr Leu Gln Glu Pro Leu Ser Asp Cys Glu	
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Glu Val Leu Cys	
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&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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Arg Cys Gln Gly Trp Lys Asn Thr Pro Leu Ser Gln Val Lys Phe Tyr  
 35 40 45

Arg Asp Gly Lys Phe Leu His Phe Ser Lys Glu Asn Gln Thr Leu Ser  
 50 55 60

Met Gly Ala Ala Thr Val Gln Ser Arg Gly Gln Tyr Ser Cys Ser Gly  
 65 70 75 80

Gln Val Met Tyr Ile Pro Gln Thr Phe Thr Gln Thr Ser Glu Thr Ala  
 85 90 95

Met Val Gln Val Gln Glu Leu Phe Pro Pro Pro Val Leu Ser Ala Ile  
 100 105 110

Pro Ser Pro Glu Pro Arg Glu Gly Ser Leu Val Thr Leu Arg Cys Gln  
 115 120 125

Thr Lys Leu His Pro Leu Arg Ser Ala Leu Arg Leu Leu Phe Ser Phe  
 130 135 140

His Lys Asp Gly His Thr Leu Gln Asp Arg Gly Pro His Pro Glu Leu  
 145 150 155 160

Cys Ile Pro Gly Ala Lys Glu Gly Asp Ser Gly Leu Tyr Trp Cys Glu  
 165 170 175

Val Ala Pro Glu Gly Gly Gln Val Gln Lys Gln Ser Pro Gln Leu Glu  
 180 185 190

Val Arg Val Gln Ala Pro Val Ser Arg Pro Val Leu Thr Leu His His  
 195 200 205

Gly Pro Ala Asp Pro Ala Val Gly Asp Met Val Gln Leu Leu Cys Glu  
 210 215 220

Ala Gln Arg Gly Ser Pro Pro Ile Leu Tyr Ser Phe Tyr Leu Asp Glu  
 225 230 235 240

Lys Ile Val Gly Asn His Ser Ala Pro Cys Gly Gly Thr Thr Ser Leu  
 245 250 255

Leu Phe Pro Val Lys Ser Glu Gln Asp Ala Gly Asn Tyr Ser Cys Glu  
 260 265 270

Ala Glu Asn Ser Val Ser Arg Glu Arg Ser Glu Pro Lys Lys Leu Ser  
 275 280 285

Leu Lys Gly Ser Gln Val Leu Phe Thr Pro Ala Ser Asn Trp Leu Val  
 290 295 300

Pro Trp Leu Pro Ala Ser Leu Leu Gly Leu Met Val Ile Ala Ala Ala  
 305 310 315 320

Leu Leu Val Tyr Val Arg Ser Trp Arg Lys Ala Gly Pro Leu Pro Ser  
 325 330 335

Gln Ile Pro Pro Thr Ala Pro Gly Gly Glu Gln Cys Pro Leu Tyr Ala  
 340 345 350

Asn Val His His Gln Lys Gly Lys Asp Glu Gly Val Val Tyr Ser Val  
 355 360 365

Val His Arg Thr Ser Lys Arg Ser Glu Ala Arg Ser Ala Glu Phe Thr  
 370 375 380

Val Gly Arg Lys Asp Ser Ser Ile Ile Cys Ala Glu Val Arg Cys Leu  
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Gln Pro Ser Glu Val Ser Ser Thr Glu Val Asn Met Arg Ser Arg Thr  
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 <213> Homo sapiens

<220>  
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 <222> (88)..(1410)  
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 Met Leu Pro Ser Leu Gly Pro Met Leu  
 1 5  
 ctc tgg acg gct gtg ctg ctc ttt gtt ccc tgt gtt ggg aaa act gtc 162  
 Leu Trp Thr Ala Val Leu Leu Phe Val Pro Cys Val Gly Lys Thr Val  
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Trp Leu Tyr Leu Gln Ala Trp Pro Asn Pro Val Phe Glu Gly Asp Ala	
30 35 40	
ctg act ctg cga tgt cag gga tgg aag aat aca cca ctg tct cag gtg	258
Leu Thr Leu Arg Cys Gln Gly Trp Lys Asn Thr Pro Leu Ser Gln Val	
45 50 55	
aag ttc tac aga gat gga aaa ttc ctt cat ttc tct aag gaa aac cag	306
Lys Phe Tyr Arg Asp Gly Lys Phe Leu His Phe Ser Lys Glu Asn Gln	
60 65 70	
act ctg tcc atg gga gca gca aca gtg cag agc cgt ggc cag tac agc	354
Thr Leu Ser Met Gly Ala Ala Thr Val Gln Ser Arg Gly Gln Tyr Ser	
75 80 85	
tgc tct ggg cag gtg atg tat att cca cag aca ttc aca caa act tca	402
Cys Ser Gly Gln Val Met Tyr Ile Pro Gln Thr Phe Thr Gln Thr Ser	
90 95 100 105	
gag act gcc atg gtt caa gtc caa gag ctg ttt cca cct cct gtg ctg	450
Glu Thr Ala Met Val Gln Val Gln Glu Leu Phe Pro Pro Pro Val Leu	
110 115 120	
agt gcc atc ccc tct cct gag ccc cga gag ggt agc ctg gtg acc ctg	498
Ser Ala Ile Pro Ser Pro Glu Pro Arg Glu Gly Ser Leu Val Thr Leu	
125 130 135	
aga tgt cag aca aag ctg cac ccc ctg agg tca gcc ttg agg ctc ctt	546
Arg Cys Gln Thr Lys Leu His Pro Leu Arg Ser Ala Leu Arg Leu Leu	
140 145 150	
ttc tcc ttc cac aag gac ggc cac acc ttg cag gac agg ggc cct cac	594
Phe Ser Phe His Lys Asp Gly His Thr Leu Gln Asp Arg Gly Pro His	
155 160 165	

cca gaa ctc tgc atc ccg gga gcc aag gag gga gac tct ggg ctt tac	642
Pro Glu Leu Cys Ile Pro Gly Ala Lys Glu Gly Asp Ser Gly Leu Tyr	
170 175 180 185	
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Trp Cys Glu Val Ala Pro Glu Gly Gly Gln Val Gln Lys Gln Ser Pro	
190 195 200	
cag ctg gag gtc aga gtg cag gct cct gta tcc cgt cct gtg ctc act	738
Gln Leu Glu Val Arg Val Gln Ala Pro Val Ser Arg Pro Val Leu Thr	
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ctg cac cac ggg cct gct gac ccc gct gtg ggg gac atg gtg cag ctc	786
Leu His His Gly Pro Ala Asp Pro Ala Val Gly Asp Met Val Gln Leu	
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ctc tgt gag gca cag agg ggc tcc cct ccg atc ctg tat tcc ttc tac	834
Leu Cys Glu Ala Gln Arg Gly Ser Pro Pro Ile Leu Tyr Ser Phe Tyr	
235 240 245	
ctt gat gag aag att gtg ggg aac cac tca gct ccc tgt ggt gga acc	882
Leu Asp Glu Lys Ile Val Gly Asn His Ser Ala Pro Cys Gly Gly Thr	
250 255 260 265	
acc tcc ctc ctc ttc cca gtg aag tca gaa cag gat gct ggg aac tac	930
Thr Ser Leu Leu Phe Pro Val Lys Ser Glu Gln Asp Ala Gly Asn Tyr	
270 275 280	
tcc tgc gag gct gag aac agt gtc tcc aga gag agg agt gag ccc aag	978
Ser Cys Glu Ala Glu Asn Ser Val Ser Arg Glu Arg Ser Glu Pro Lys	
285 290 295	
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Lys Leu Ser Leu Lys Gly Ser Gln Val Leu Phe Thr Pro Ala Ser Asn	
300 305 310	

tgg ctg gtt cct tgg ctt cct gcg agc ctg ctt ggc ctg atg gtt att	1074
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315 320 325	
gct gct gca ctt ctg gtt tat gtg aga tcc tgg aga aaa gct ggg ccc	1122
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ctt cca tcc cag ata cca ccc aca gct cca ggt gga gag cag tgc cca	1170
Leu Pro Ser Gln Ile Pro Pro Thr Ala Pro Gly Gly Glu Gln Cys Pro	
350 355 360	
cta tat gcc aac gtg cat cac cag aaa ggg aaa gat gaa ggt gtt gtc	1218
Leu Tyr Ala Asn Val His His Gln Lys Gly Lys Asp Glu Gly Val Val	
365 370 375	
tac tct gtg gtg cat aga acc tca aag agg agt gaa gcc agg tct gct	1266
Tyr Ser Val Val His Arg Thr Ser Lys Arg Ser Glu Ala Arg Ser Ala	
380 385 390	
gag ttc acc gtg ggg aga aag gac agt tct atc atc tgt gcg gag gtg	1314
Glu Phe Thr Val Gly Arg Lys Asp Ser Ser Ile Ile Cys Ala Glu Val	
395 400 405	
aga tgc ctg cag ccc agt gag gtt tca tcc acg gag gtg aat atg aga	1362
Arg Cys Leu Gln Pro Ser Glu Val Ser Ser Thr Glu Val Asn Met Arg	
410 415 420 425	
agc agg act ctc caa gaa ccc ctt agc gac tgt gag gag gtt ctc tgc	1410
Ser Arg Thr Leu Gln Glu Pro Leu Ser Asp Cys Glu Glu Val Leu Cys	
430 435 440	
tagtgatggt gttctcctat caacacacgc ccacccccag tctccagtgc tctcaggaa	1470
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<211> 441

<212> PRT

<213> Homo sapiens

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Pro Asn Pro Val Phe Glu Gly Asp Ala Leu Thr Leu Arg Cys Gln Gly  
 35 40 45

Trp Lys Asn Thr Pro Leu Ser Gln Val Lys Phe Tyr Arg Asp Gly Lys  
 50 55 60

Phe Leu His Phe Ser Lys Glu Asn Gln Thr Leu Ser Met Gly Ala Ala  
 65 70 75 80

Thr Val Gln Ser Arg Gly Gln Tyr Ser Cys Ser Gly Gln Val Met Tyr  
 85 90 95

Ile Pro Gln Thr Phe Thr Gln Thr Ser Glu Thr Ala Met Val Gln Val  
 100 105 110

Gln Glu Leu Phe Pro Pro Pro Val Leu Ser Ala Ile Pro Ser Pro Glu  
 115 120 125

Pro Arg Glu Gly Ser Leu Val Thr Leu Arg Cys Gln Thr Lys Leu His  
 130 135 140

Pro Leu Arg Ser Ala Leu Arg Leu Leu Phe Ser Phe His Lys Asp Gly  
 145 150 155 160

His Thr Leu Gln Asp Arg Gly Pro His Pro Glu Leu Cys Ile Pro Gly  
 165 170 175

Ala Lys Glu Gly Asp Ser Gly Leu Tyr Trp Cys Glu Val Ala Pro Glu  
 180 185 190

Gly Gly Gln Val Gln Lys Gln Ser Pro Gln Leu Glu Val Arg Val Gln  
 195 200 205

Ala Pro Val Ser Arg Pro Val Leu Thr Leu His His Gly Pro Ala Asp  
 210 215 220

Pro Ala Val Gly Asp Met Val Gln Leu Leu Cys Glu Ala Gln Arg Gly  
 225 230 235 240

Ser Pro Pro Ile Leu Tyr Ser Phe Tyr Leu Asp Glu Lys Ile Val Gly  
 245 250 255

Asn His Ser Ala Pro Cys Gly Gly Thr Thr Ser Leu Leu Phe Pro Val

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265

270

Lys Ser Glu Gln Asp Ala Gly Asn Tyr Ser Cys Glu Ala Glu Asn Ser

275

280

285

Val Ser Arg Glu Arg Ser Glu Pro Lys Lys Leu Ser Leu Lys Gly Ser

290

295

300

Gln Val Leu Phe Thr Pro Ala Ser Asn Trp Leu Val Pro Trp Leu Pro

305

310

315

320

Ala Ser Leu Leu Gly Leu Met Val Ile Ala Ala Ala Leu Leu Val Tyr

325

330

335

Val Arg Ser Trp Arg Lys Ala Gly Pro Leu Pro Ser Gln Ile Pro Pro

340

345

350

Thr Ala Pro Gly Gly Glu Gln Cys Pro Leu Tyr Ala Asn Val His His

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360

365

Gln Lys Gly Lys Asp Glu Gly Val Val Tyr Ser Val Val His Arg Thr

370

375

380

Ser Lys Arg Ser Glu Ala Arg Ser Ala Glu Phe Thr Val Gly Arg Lys

385

390

395

400

Asp Ser Ser Ile Ile Cys Ala Glu Val Arg Cys Leu Gln Pro Ser Glu

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410

415

Val Ser Ser Thr Glu Val Asn Met Arg Ser Arg Thr Leu Gln Glu Pro

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425

430

Leu Ser Asp Cys Glu Glu Val Leu Cys

435

440

&lt;210&gt; 5

&lt;211&gt; 1543

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (115)..(921)

&lt;223&gt;

&lt;400&gt; 5

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Met

1

ctg ctc tgg atg gtt ctc ctg ctc tgt gat tcc atg gtt gaa gct caa 165

Leu Leu Trp Met Val Leu Leu Leu Cys Asp Ser Met Val Glu Ala Gln

5

10

15

gag ttg ttc cca aat cct gag ctg aca gaa ttc acc aat tca gag acg 213

Glu Leu Phe Pro Asn Pro Glu Leu Thr Glu Phe Thr Asn Ser Glu Thr

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25

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atg gat gtc atc ctg aag tgt acc ata aag gtg gac ccc aag aat cca 261

Met Asp Val Ile Leu Lys Cys Thr Ile Lys Val Asp Pro Lys Asn Pro

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act tta cag ctc ttt tac act ttc tac aag gac aac cat gtc att caa 309

Thr Leu Gln Leu Phe Tyr Thr Phe Tyr Lys Asp Asn His Val Ile Gln

50

55

60

65

gac agg agt ccc cac tca gta ttt tct gca gaa gcc aag gag gaa aac	357
Asp Arg Ser Pro His Ser Val Phe Ser Ala Glu Ala Lys Glu Glu Asn	
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tct ggg ctc tac cag tgt atg gtg gac act gag gat ggc tta att cag	405
Ser Gly Leu Tyr Gln Cys Met Val Asp Thr Glu Asp Gly Leu Ile Gln	
85 90 95	
aaa aaa agt ggc tat ctg gat atc cag ttc tgg act cct gta tcc cat	453
Lys Lys Ser Gly Tyr Leu Asp Ile Gln Phe Trp Thr Pro Val Ser His	
100 105 110	
cct gtg ctc act ctg caa cat gaa gcc act aac ctt gct gta gga gac	501
Pro Val Leu Thr Leu Gln His Glu Ala Thr Asn Leu Ala Val Gly Asp	
115 120 125	
aag gtg gag ttc ctc tgt gag gcc cac cag ggc tcc ctt cca atc ttt	549
Lys Val Glu Phe Leu Cys Glu Ala His Gln Gly Ser Leu Pro Ile Phe	
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Tyr Ser Phe Tyr Ile Asn Gly Glu Ile Leu Gly Lys Pro Leu Ala Pro	
150 155 160	
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Ser Gly Arg Ala Ala Ser Leu Leu Ala Ser Val Lys Ala Glu Trp Ser	
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acc aag aac tat tcc tgt gaa gct aaa aac aac atc tcc aga gaa ata	693
Thr Lys Asn Tyr Ser Cys Glu Ala Lys Asn Asn Ile Ser Arg Glu Ile	
180 185 190	
agt gag ctc aag aag ttc ccc ttg gtt gtc tca ggt act gcc tgg atc	741
Ser Glu Leu Lys Lys Phe Pro Leu Val Val Ser Gly Thr Ala Trp Ile	
195 200 205	

aag agc aac atg cta act atc tgg cta cct gca agc ctg ctt gga ggg	789
Lys Ser Asn Met Leu Thr Ile Trp Leu Pro Ala Ser Leu Leu Gly Gly	
210 215 220 225	
atg gtc att gcg gct gtg gtt cta atg tat ttc ttc aaa ccc tgt aaa	837
Met Val Ile Ala Ala Val Val Leu Met Tyr Phe Phe Lys Pro Cys Lys	
230 235 240	
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Lys His Ala Arg Pro Glu Met Pro Thr Leu Lys Glu Pro Asp Ser Phe	
245 250 255	
cta tat gta tcg gtt gat aat cga aga tat aaa tga gattcccacc	931
Leu Tyr Val Ser Val Asp Asn Arg Arg Tyr Lys	
260 265	
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taagatacga ta

1543

&lt;210&gt; 6

&lt;211&gt; 268

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 6

Met Leu Leu Trp Met Val Leu Leu Leu Cys Asp Ser Met Val Glu Ala

1

5

10

15

Gln Glu Leu Phe Pro Asn Pro Glu Leu Thr Glu Phe Thr Asn Ser Glu

20

25

30

Thr Met Asp Val Ile Leu Lys Cys Thr Ile Lys Val Asp Pro Lys Asn

35

40

45

Pro Thr Leu Gln Leu Phe Tyr Thr Phe Tyr Lys Asp Asn His Val Ile

50

55

60

Gln Asp Arg Ser Pro His Ser Val Phe Ser Ala Glu Ala Lys Glu Glu

65

70

75

80

Asn Ser Gly Leu Tyr Gln Cys Met Val Asp Thr Glu Asp Gly Leu Ile

85

90

95

Gln Lys Lys Ser Gly Tyr Leu Asp Ile Gln Phe Trp Thr Pro Val Ser

100

105

110

His Pro Val Leu Thr Leu Gln His Glu Ala Thr Asn Leu Ala Val Gly

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120

125

Asp Lys Val Glu Phe Leu Cys Glu Ala His Gln Gly Ser Leu Pro Ile

130

135

140

Phe Tyr Ser Phe Tyr Ile Asn Gly Glu Ile Leu Gly Lys Pro Leu Ala  
 145 150 155 160

Pro Ser Gly Arg Ala Ala Ser Leu Leu Ala Ser Val Lys Ala Glu Trp  
 165 170 175

Ser Thr Lys Asn Tyr Ser Cys Glu Ala Lys Asn Asn Ile Ser Arg Glu  
 180 185 190

Ile Ser Glu Leu Lys Lys Phe Pro Leu Val Val Ser Gly Thr Ala Trp  
 195 200 205

Ile Lys Ser Asn Met Leu Thr Ile Trp Leu Pro Ala Ser Leu Leu Gly  
 210 215 220

Gly Met Val Ile Ala Ala Val Val Leu Met Tyr Phe Phe Lys Pro Cys  
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Lys Lys His Ala Arg Pro Glu Met Pro Thr Leu Lys Glu Pro Asp Ser  
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Phe Leu Tyr Val Ser Val Asp Asn Arg Arg Tyr Lys  
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<211> 34

<212> DNA

<213> Artificial

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IAP5 Rec'd PCT/PTO 28 MAR 2006

<110> Matsushima, Kouji  
 Hashimoto, Shinichi  
 Tsuchiya, Masayuki  
 Hirata, Yuichi  
 Yoshida, Kenji  
 Ojima, Kazuyuki

<120> PROTEIN EXPRESSED IN NK CELL

<130> 14875-157US1

<150> PCT/JP2004/14207

<151> 2004-09-29

<150> JP 2003-338331

<151> 2003-09-29

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<170> PatentIn version 3.1

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Glu Gly Asp Ala Leu Thr Leu Arg Cys Gln Gly Trp Lys Asn Thr Pro

30 35 40

ctg tct cag gtg aag ttc tac aga gat gga aaa ttc ctt cat ttc tct 257

Leu Ser Gln Val Lys Phe Tyr Arg Asp Gly Lys Phe Leu His Phe Ser

45 50 55

aag gaa aac cag act ctg tcc atg gga gca gca aca gtg cag agc cgt 305

Lys Glu Asn Gln Thr Leu Ser Met Gly Ala Ala Thr Val Gln Ser Arg

60 65 70

ggc cag tac agc tgc tct ggg cag gtg atg tat att cca cag aca ttc 353

Gly Gln Tyr Ser Cys Ser Gly Gln Val Met Tyr Ile Pro Gln Thr Phe

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ctg gtg acc ctg aga tgt cag aca aag ctg cac ccc ctg agg tca gcc Leu Val Thr Leu Arg Cys Gln Thr Lys Leu His Pro Leu Arg Ser Ala 125 130 135			497
ttg agg ctc ctt ttc tcc ttc cac aag gac ggc cac acc ttg cag gac Leu Arg Leu Leu Phe Ser Phe His Lys Asp Gly His Thr Leu Gln Asp 140 145 150			545
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cct gtg ctc act ctg cac cac ggg cct gct gac cct gct gtg ggg gac Pro Val Leu Thr Leu His His Gly Pro Ala Asp Pro Ala Val Gly Asp 205 210 215			737
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gct ggg aac tac tcc tgc gag gct gag aac agt gtc tcc aga gag agg Ala Gly Asn Tyr Ser Cys Glu Ala Glu Asn Ser Val Ser Arg Glu Arg 270 275 280			929
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aaa gct ggg ccc ctt cca tcc cag ata cca ccc aca gct cca ggt gga 1121  
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gaa ggt gtt gtc tac tct gtg gtg cat aga acc tca aag agg agt gaa 1217  
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 Cys Ala Glu Val Arg Cys Leu Gln Pro Ser Glu Val Ser Ser Thr Glu  
 395 400 405

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 410 415 420 425

gag gtt ctc tgc tag tgatggtgtt ctctatcaa cacacgccca ccccgagtct 1416  
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 35 40 45  
 Arg Asp Gly Lys Phe Leu His Phe Ser Lys Glu Asn Gln Thr Leu Ser  
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 Met Gly Ala Ala Thr Val Gln Ser Arg Gly Gln Tyr Ser Cys Ser Gly  
 65 70 75 80

Gln	Val	Met	Tyr	Ile	Pro	Gln	Thr	Phe	Thr	Gln	Thr	Ser	Glu	Thr	Ala	
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Pro	Ser	Pro	Glu	Pro	Arg	Glu	Gly	Ser	Leu	Val	Thr	Leu	Arg	Cys	Gln	
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Cys	Ile	Pro	Gly	Ala	Lys	Glu	Gly	Asp	Ser	Gly	Leu	Tyr	Trp	Cys	Glu	
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Val	Ala	Pro	Glu	Gly	Gly	Gln	Val	Gln	Lys	Gln	Ser	Pro	Gln	Leu	Glu	
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ctc tgg acg gct gtg ctg ctc ttt gtt ccc tgt gtt ggg aaa act gtc 162  
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Arg	Cys	Gln	Thr	Lys	Leu	His	Pro	Leu	Arg	Ser	Ala	Leu	Arg	Leu	Leu	
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Ser	Cys	Glu	Ala	Glu	Asn	Ser	Val	Ser	Arg	Glu	Arg	Ser	Glu	Pro	Lys	
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Lys	Leu	Ser	Leu	Lys	Gly	Ser	Gln	Val	Leu	Phe	Thr	Pro	Ala	Ser	Asn	
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Trp	Leu	Val	Pro	Trp	Leu	Pro	Ala	Ser	Leu	Leu	Gly	Leu	Met	Val	Ile	
315						320				325						
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Ala	Ala	Ala	Leu	Leu	Val	Tyr	Val	Arg	Ser	Trp	Arg	Lys	Ala	Gly	Pro	
330				335						340				345		
ctt	cca	tcc	cag	ata	cca	ccc	aca	gct	cca	ggt	gga	gag	cag	tgc	cca	1170
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Pro Asn Pro Val Phe Glu Gly Asp Ala Leu Thr Leu Arg Cys Gln Gly  
35 40 45

Trp Lys Asn Thr Pro Leu Ser Gln Val Lys Phe Tyr Arg Asp Gly Lys  
 50 55 60  
 Phe Leu His Phe Ser Lys Glu Asn Gln Thr Leu Ser Met Gly Ala Ala  
 65 70 75 80  
 Thr Val Gln Ser Arg Gly Gln Tyr Ser Cys Ser Gly Gln Val Met Tyr  
 85 90 95  
 Ile Pro Gln Thr Phe Thr Gln Thr Ser Glu Thr Ala Met Val Gln Val  
 100 105 110  
 Gln Glu Leu Phe Pro Pro Pro Val Leu Ser Ala Ile Pro Ser Pro Glu  
 115 120 125  
 Pro Arg Glu Gly Ser Leu Val Thr Leu Arg Cys Gln Thr Lys Leu His  
 130 135 140  
 Pro Leu Arg Ser Ala Leu Arg Leu Leu Phe Ser Phe His Lys Asp Gly  
 145 150 155 160  
 His Thr Leu Gln Asp Arg Gly Pro His Pro Glu Leu Cys Ile Pro Gly  
 165 170 175  
 Ala Lys Glu Gly Asp Ser Gly Leu Tyr Trp Cys Glu Val Ala Pro Glu  
 180 185 190  
 Gly Gly Gln Val Gln Lys Gln Ser Pro Gln Leu Glu Val Arg Val Gln  
 195 200 205  
 Ala Pro Val Ser Arg Pro Val Leu Thr Leu His His Gly Pro Ala Asp  
 210 215 220  
 Pro Ala Val Gly Asp Met Val Gln Leu Leu Cys Glu Ala Gln Arg Gly  
 225 230 235 240  
 Ser Pro Pro Ile Leu Tyr Ser Phe Tyr Leu Asp Glu Lys Ile Val Gly  
 245 250 255  
 Asn His Ser Ala Pro Cys Gly Gly Thr Thr Ser Leu Leu Phe Pro Val  
 260 265 270  
 Lys Ser Glu Gln Asp Ala Gly Asn Tyr Ser Cys Glu Ala Glu Asn Ser  
 275 280 285  
 Val Ser Arg Glu Arg Ser Glu Pro Lys Lys Leu Ser Leu Lys Gly Ser  
 290 295 300  
 Gln Val Leu Phe Thr Pro Ala Ser Asn Trp Leu Val Pro Trp Leu Pro  
 305 310 315 320  
 Ala Ser Leu Leu Gly Leu Met Val Ile Ala Ala Ala Leu Leu Val Tyr  
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 Val Arg Ser Trp Arg Lys Ala Gly Pro Leu Pro Ser Gln Ile Pro Pro

340	345	350
Thr Ala Pro Gly Gly Glu Gln Cys Pro Leu Tyr Ala Asn Val His His		
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Gln Lys Gly Lys Asp Glu Gly Val Val Tyr Ser Val Val His Arg Thr		
370	375	380
Ser Lys Arg Ser Glu Ala Arg Ser Ala Glu Phe Thr Val Gly Arg Lys		
385	390	395
Asp Ser Ser Ile Ile Cys Ala Glu Val Arg Cys Leu Gln Pro Ser Glu		
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Val Ser Ser Thr Glu Val Asn Met Arg Ser Arg Thr Leu Gln Glu Pro		
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	Met
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ctg ctc tgg atg gtt ctc ctg ctc tgt gat tcc atg gtt gaa gct caa	165
Leu Leu Trp Met Val Leu Leu Leu Cys Asp Ser Met Val Glu Ala Gln	
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gag ttg ttc cca aat cct gag ctg aca gaa ttc acc aat tca gag acg	213
Glu Leu Phe Pro Asn Pro Glu Leu Thr Glu Phe Thr Asn Ser Glu Thr	
20	25
atg gat gtc atc ctg aag tgt acc ata aag gtg gac ccc aag aat cca	261
Met Asp Val Ile Leu Lys Cys Thr Ile Lys Val Asp Pro Lys Asn Pro	
35	40
act tta cag ctc ttt tac act ttc tac aag gac aac cat gtc att caa	309
Thr Leu Gln Leu Phe Tyr Thr Phe Tyr Lys Asp Asn His Val Ile Gln	
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gac agg agt ccc cac tca gta ttt tct gca gaa gcc aag gag gaa aac	357
Asp Arg Ser Pro His Ser Val Phe Ser Ala Glu Ala Lys Glu Glu Asn	
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	80

tct ggg ctc tac cag tgt atg gtg gac act gag gat ggc tta att cag	405
Ser Gly Leu Tyr Gln Cys Met Val Asp Thr Glu Asp Gly Leu Ile Gln	
85 90 95	
aaa aaa agt ggc tat ctg gat atc cag ttc tgg act cct gta tcc cat	453
Lys Lys Ser Gly Tyr Leu Asp Ile Gln Phe Trp Thr Pro Val Ser His	
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cct gtg ctc act ctg caa cat gaa gcc act aac ctt gct gta gga gac	501
Pro Val Leu Thr Leu Gln His Glu Ala Thr Asn Leu Ala Val Gly Asp	
115 120 125	
aag gtg gag ttc ctc tgt gag gcc cac cag ggc tcc ctt cca atc ttt	549
Lys Val Glu Phe Leu Cys Glu Ala His Gln Gly Ser Leu Pro Ile Phe	
130 135 140 145	
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Tyr Ser Phe Tyr Ile Asn Gly Glu Ile Leu Gly Lys Pro Leu Ala Pro	
150 155 160	
tct ggc aga gct gcc tcc ctc cta gcc tca gta aag gca gag tgg agt	645
Ser Gly Arg Ala Ala Ser Leu Leu Ala Ser Val Lys Ala Glu Trp Ser	
165 170 175	
acc aag aac tat tcc tgt gaa gct aaa aac aac atc tcc aga gaa ata	693
Thr Lys Asn Tyr Ser Cys Glu Ala Lys Asn Asn Ile Ser Arg Glu Ile	
180 185 190	
agt gag ctc aag aag ttc ccc ttg gtt gtc tca ggt act gcc tgg atc	741
Ser Glu Leu Lys Lys Phe Pro Leu Val Val Ser Gly Thr Ala Trp Ile	
195 200 205	
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Lys Ser Asn Met Leu Thr Ile Trp Leu Pro Ala Ser Leu Leu Gly Gly	
210 215 220 225	
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Met Val Ile Ala Ala Val Val Leu Met Tyr Phe Phe Lys Pro Cys Lys	
230 235 240	
aag cat gcc aga cct gag atg ccc acc cta aaa gag cca gac agt ttt	885
Lys His Ala Arg Pro Glu Met Pro Thr Leu Lys Glu Pro Asp Ser Phe	
245 250 255	
cta tat gta tcg gtt gat aat cga aga tat aaa tga gattcccacc	931
Leu Tyr Val Ser Val Asp Asn Arg Arg Tyr Lys	
260 265	
aatgatttgg attcaaaaac caggacctgc caagatcccc ttggtcttta ggatcatgct	991
ctgtgttagt gcaatgtctt cctccagcat atactcaact ccagctccca gcctccaccc	1051
tccagcactc agcagtggtt ccaagttctc cctgcaggtc acccagttcc tagcccagca	1111
gtgaggaagc ccatatgctc tattcctggc cagggctcct gaactgtggg ttctcttctg	1171
agcgggaaac caaacaatgg tgtgggaatg aacaatttcc accttgatac atacatatac	1231

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 Thr Met Asp Val Ile Leu Lys Cys Thr Ile Lys Val Asp Pro Lys Asn  
 35 40 45  
 Pro Thr Leu Gln Leu Phe Tyr Thr Phe Tyr Lys Asp Asn His Val Ile  
 50 55 60  
 Gln Asp Arg Ser Pro His Ser Val Phe Ser Ala Glu Ala Lys Glu Glu  
 65 70 75 80  
 Asn Ser Gly Leu Tyr Gln Cys Met Val Asp Thr Glu Asp Gly Leu Ile  
 85 90 95  
 Gln Lys Lys Ser Gly Tyr Leu Asp Ile Gln Phe Trp Thr Pro Val Ser  
 100 105 110  
 His Pro Val Leu Thr Leu Gln His Glu Ala Thr Asn Leu Ala Val Gly  
 115 120 125  
 Asp Lys Val Glu Phe Leu Cys Glu Ala His Gln Gly Ser Leu Pro Ile  
 130 135 140  
 Phe Tyr Ser Phe Tyr Ile Asn Gly Glu Ile Leu Gly Lys Pro Leu Ala  
 145 150 155 160  
 Pro Ser Gly Arg Ala Ala Ser Leu Leu Ala Ser Val Lys Ala Glu Trp  
 165 170 175  
 Ser Thr Lys Asn Tyr Ser Cys Glu Ala Lys Asn Asn Ile Ser Arg Glu  
 180 185 190

Ile Ser Glu Leu Lys Lys Phe Pro Leu Val Val Ser Gly Thr Ala Trp  
 195 200 205

Ile Lys Ser Asn Met Leu Thr Ile Trp Leu Pro Ala Ser Leu Leu Gly  
 210 215 220

Gly Met Val Ile Ala Ala Val Val Leu Met Tyr Phe Phe Lys Pro Cys  
 225 230 235 240

Lys Lys His Ala Arg Pro Glu Met Pro Thr Leu Lys Glu Pro Asp Ser  
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Phe Leu Tyr Val Ser Val Asp Asn Arg Arg Tyr Lys  
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cgttcgcggg cgcaactgca

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ggatccttag acgtatctcg ccgaaa

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